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Sequence Listing was accepted.

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217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=10; day=5; hr=15; min=8; sec=12; ms=280; ]

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Application No: 10550363 Version No: 2.0

Input Set:

Output Set:

Started: 2009-09-18 16:25:00.198  
Finished: 2009-09-18 16:25:01.941  
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 743 ms  
Total Warnings: 13  
Total Errors: 0  
No. of SeqIDs Defined: 20  
Actual SeqID Count: 20

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

# SEQUENCE LISTING

<110> Glaxo Group Limited  
VINSON, Mary  
IRVING, Elaine Alison

<120> THERAPEUTICAL USE OF ANTI-MYELIN  
ASSOCIATED GLYCOPROTEIN (MAG) ANTIBODIES

<130> PB60024

<140> 10550363  
<141> 2009-09-18

<150> PCT/EP2004/001016  
<151> 2004-02-02

<150> 0306309.6  
<151> 2003-03-19

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 17  
<212> PRT  
<213> MUS MUSCULUS

<400> 1  
Lys Ser Ser His Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu  
1 5 10 15  
Ala

<210> 2  
<211> 7  
<212> PRT  
<213> MUS MUSCULUS

<400> 2  
Trp Ala Ser Thr Arg Glu Ser  
1 5

<210> 3  
<211> 8  
<212> PRT  
<213> MUS MUSCULUS

<400> 3  
His Gln Tyr Leu Ser Ser Leu Thr  
1 5

<210> 4  
<211> 5  
<212> PRT  
<213> MUS MUSCULUS

<400> 4  
Asn Tyr Gly Met Asn  
1 5

<210> 5  
<211> 17  
<212> PRT  
<213> MUS MUSCULUS

<400> 5  
Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Thr  
1 5 10 15  
Gly

<210> 6  
<211> 17  
<212> PRT  
<213> MUS MUSCULUS

<400> 6  
Asn Pro Ile Asn Tyr Tyr Gly Ile Asn Tyr Glu Gly Tyr Val Met Asp  
1 5 10 15  
Tyr

<210> 7  
<211> 475  
<212> PRT  
<213> MUS MUSCULUS

<400> 7  
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15  
Val His Ser Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys  
20 25 30  
Pro Gly Glu Thr Asn Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45  
Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu  
50 55 60  
Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala  
65 70 75 80  
Asp Asp Phe Thr Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser  
85 90 95  
Thr Ala Tyr Leu Gln Ile Ser Asn Leu Lys Asn Glu Asp Thr Ala Thr  
100 105 110  
Tyr Phe Cys Ala Arg Asn Pro Ile Asn Tyr Tyr Gly Ile Asn Tyr Glu

115	120	125
Gly Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser		
130	135	140
Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser		
145	150	155
Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp		
165	170	175
Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr		
180	185	190
Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr		
195	200	205
Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln		
210	215	220
Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp		
225	230	235
Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro		
245	250	255
Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser Val Phe Leu Phe Pro		
260	265	270
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr		
275	280	285
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn		
290	295	300
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg		
305	310	315
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val		
325	330	335
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser		
340	345	350
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys		
355	360	365
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp		
370	375	380
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe		
385	390	395
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu		
405	410	415
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe		
420	425	430
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly		
435	440	445
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr		
450	455	460
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		
465	470	475

<210> 8

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain

<400> 8

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1		5		10		15									
Val	His	Ser	Asn	Ile	Met	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ala	Val
		20						25					30		
Ser	Ala	Gly	Glu	Lys	Val	Thr	Met	Ser	Cys	Lys	Ser	Ser	His	Ser	Val
	35						40					45			
Leu	Tyr	Ser	Ser	Asn	Gln	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys
	50					55					60				
Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu
65					70					75				80	
Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe
				85					90					95	
Thr	Leu	Thr	Ile	Ile	Asn	Val	His	Thr	Glu	Asp	Leu	Ala	Val	Tyr	Tyr
			100					105					110		
Cys	His	Gln	Tyr	Leu	Ser	Ser	Leu	Thr	Phe	Gly	Thr	Gly	Thr	Lys	Leu
	115						120					125			
Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro
	130					135					140				
Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu
145					150					155				160	
Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn
			165					170						175	
Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser
		180						185					190		
Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala
	195					200						205			
Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly
	210					215					220				
Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys		
225					230					235					

<210> 9

<211> 475

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 9

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1				5					10					15	
Val	His	Ser	Glu	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	Leu	Lys	Lys
		20						25					30		
Pro	Gly	Glu	Thr	Asn	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
	35					40						45			
Thr	Asn	Tyr	Gly	Met	Asn	Trp	Val	Lys	Gln	Ala	Pro	Gly	Lys	Gly	Leu
	50				55						60				
Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	Ala
65					70					75				80	
Asp	Asp	Phe	Thr	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Thr	Ser	Ala	Ser
			85						90					95	
Thr	Ala	Tyr	Leu	Gln	Ile	Ser	Asn	Leu	Lys	Asn	Glu	Asp	Thr	Ala	Thr
		100						105						110	
Tyr	Phe	Cys	Ala	Arg	Asn	Pro	Ile	Asn	Tyr	Tyr	Gly	Ile	Asn	Tyr	Glu
	115					120						125			
Gly	Tyr	Val	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser

130		135		140	
Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser					
145		150		155	160
Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp					
	165		170		175
Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr					
	180		185		190
Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr					
	195		200		205
Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln					
	210		215		220
Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp					
225		230		235	240
Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro					
	245		250		255
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro					
	260		265		270
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr					
	275		280		285
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn					
	290		295		300
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg					
305		310		315	320
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val					
	325		330		335
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser					
	340		345		350
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys					
	355		360		365
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp					
	370		375		380
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe					
385		390		395	400
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu					
	405		410		415
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe					
	420		425		430
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly					
	435		440		445
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr					
	450		455		460
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys					
465		470		475	

<210> 10

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain variable region

<400> 10

Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala			
1	5	10	15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr			





Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	Ala	Asp	Asp	Phe
50						55					60				
Thr	Gly	Arg	Phe	Val	Phe	Ser	Leu	Asp	Thr	Ser	Val	Ser	Thr	Ala	Tyr
65					70					75					80
Leu	Gln	Ile	Ser	Ser	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys
			85					90					95		
Ala	Arg	Asn	Pro	Ile	Asn	Tyr	Tyr	Gly	Ile	Asn	Tyr	Glu	Gly	Tyr	Val
		100						105					110		
Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
		115					120						125		

<210> 13

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain variable region

<400> 13

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ser	Glu	Leu	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Asn	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr
			20					25					30		
Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	Ala	Asp	Asp	Phe
50						55					60				
Thr	Gly	Arg	Phe	Val	Phe	Ser	Leu	Asp	Thr	Ser	Val	Ser	Thr	Ala	Tyr
65					70					75					80
Leu	Gln	Ile	Ser	Ser	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys
			85					90					95		
Ala	Arg	Asn	Pro	Ile	Asn	Tyr	Tyr	Gly	Ile	Asn	Tyr	Glu	Gly	Tyr	Val
		100						105					110		
Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
		115					120						125		

<210> 14

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain variable region

<400> 14

Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val	Ser	Leu	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	His	Ser	Val	Leu	Tyr	Ser
			20					25					30		
Ser	Asn	Gln	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln
		35					40					45			
Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val
50					55						60				
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr

65		70		75		80									
Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	His	Gln
			85						90					95	
Tyr	Leu	Ser	Ser	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys
			100					105					110		
Arg	Thr	Val													
			115												

<210> 15

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain variable region

<400> 15

Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val	Ser	Leu	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	His	Ser	Val	Leu	Tyr	Ser
			20					25					30		
Ser	Asn	Gln	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln
		35				40						45			
Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val
		50				55					60				
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr
65					70					75					